

S. alba
B. napus
Soybean
Peanut
Squash
Flax
Sunflower
Safflower
Maize

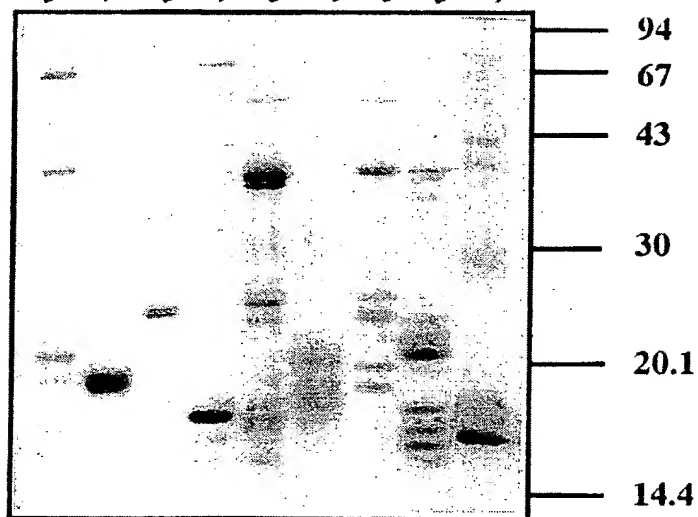
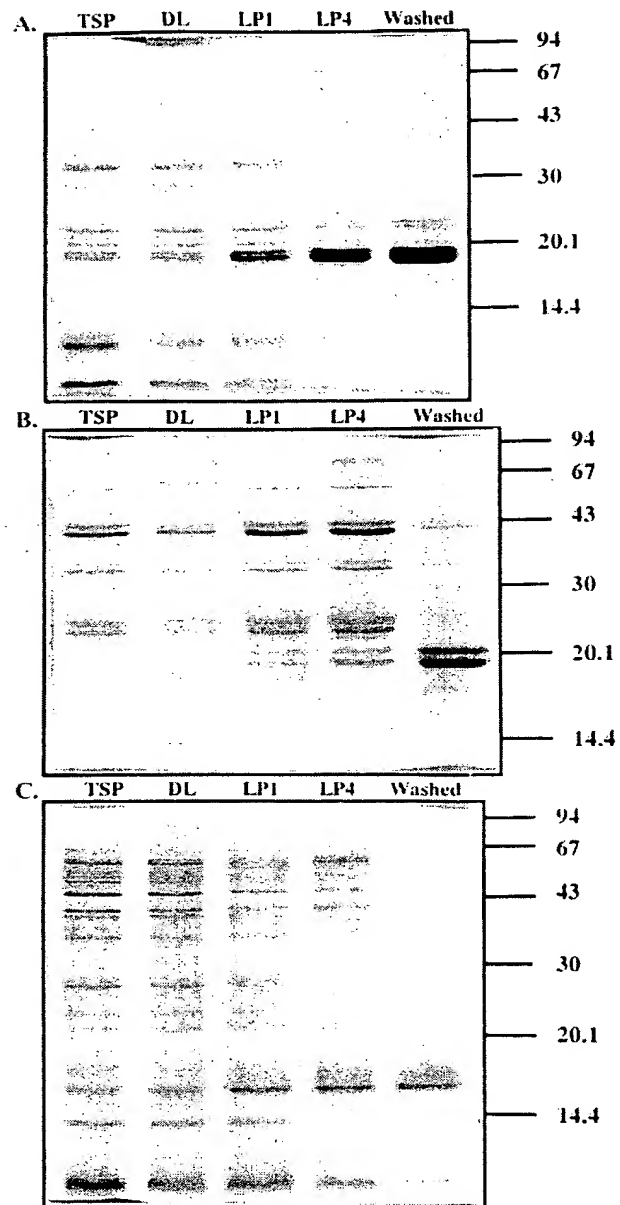


FIGURE 2



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FIGURE 3

ClustalW Formatted Alignments

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TR      10      20      30      40      50      60
ATTHIREDB ATGAA TGGTCTCGAA AACTCACAACA CAAGGCTCTGTATCGTAGGAAGTGGCC CAGCGGCA
ATGAA TGGTCTCGAA AACTCACAACA CAAGGCTCTGTATCGTAGGAAGTGGCC CAGCGGCA

TR      70      80      90      100     110     120
ATTHIREDB CACACGGCGGGGATTACGCAGCTAGGGCTGAACCTAAACCCTCTCTCTTGAAGGATGG
CACACGGCGGGGATTACGCAGCTAGGGCTGAACCTAAACCCTCTCTCTTGAAGGATGG

TR      130     140     150     160     170     180
ATTHIREDB ATGGCTAACGACATCGCTCCGGTGGTCAACTAA CACCAC CACBA CGTC GAGAATTTC
ATGGCTAACGACATCGCTCCGGTGGTCAACTAA CACCAC CACBA CGTC GAGAATTTC

TR      190     200     210     220     230     240
ATTHIREDB CCGGGATTTC CAGAAGGTAATTC CGGAGTAGAGCTGAC TGA CAAATTC CGTAAACAATCG
CCGGGATTTC CAGAAGGTAATTC CGGAGTAGAGCTGAC TGA CAAATTC CGTAAACAATCG

TR      250     260     270     280     290     300
ATTHIREDB GAGCGATTTCGGTACTACGATATTTACAGAGACGGTGACGAAAGTCGATTTCTCTTCGAAA
GAGCGATTTCGGTACTACGATATTTACAGAGACGGTGACGAAAGTCGATTTCTCTTCGAAA

TR      310     320     330     340     350     360
ATTHIREDB CCGTTTAAGCTATTCA CAGATTCAAAAAGCCATTCTCGCTGACGCTGTGATTCTCGCTAC T
CCGTTTAAGCTATTCA CAGATTCAAAAAGCCATTCTCGCTGACGCTGTGATTCTCGCTAC T

TR      370     380     390     400     410     420
ATTHIREDB CGAGCTGTGGCTAAGT GGCCTAGCTTCGTTGGATCTGGTGAAGG T T C TGGAGGTTTC TGG
GGA GCTGTGGCTAAGT GGCCTAGCTTCGTTGGATCTGGTGAAGG T T C TGGAGGTTTC TGG

TR      430     440     450     460     470     480
ATTHIREDB AACCGTGGAAATCTCCGCTTGTGCTGTTTGC GACGGAAGCTGCTCCGATATTCGGT AACCAA
AACCGTGGAAATCTCCGCTTGTGCTGTTTGC GACGGAAGCTGCTCCGATATTCGGT AACCAA

TR      490     500     510     520     530     540
ATTHIREDB CCTCTTGGCGGTGATCGGTGGAGGCGATTCT GCAATGGAAAGAAGCAAACTTTCTTACAAAA
CCTCTTGGCGGTGATCGGTGGAGGCGATTCT GCAATGGAAAGAAGCAAACTTTCTTACAAAA

TR      550     560     570     580     590     600
ATTHIREDB TATGGATCTAAAGTGTATATAATCT ATAGGAGAGATGCTTTTACAGGCTTAAAGATATG
TATGGATCTAAAGTGTATATAATCT ATAGGAGAGATGCTTTTACAGGCTTAAAGATATG

TR      610     620     630     640     650     660
ATTHIREDB CAGCAGCGAGCTTTGTCCTAATCCTAAGATTGATGTGATTGGAACCTGCTCTGTTGTGGAA
CAGCAGCGAGCTTTGTCCTAATCCTAAGATTGATGTGATTGGAACCTGCTCTGTTGTGGAA

TR      670     680     690     700     710     720
ATTHIREDB GCTTATGGA GATGGAGAAAGAGATGTGCTTGGAGGATTGAAAGTGAAGAAATGTGGTTACC
GCTTATGGA GATGGAGAAAGAGATGTGCTTGGAGGATTGAAAGTGAAGAAATGTGGTTACC

TR      730     740     750     760     770     780
ATTHIREDB GGA GATGTTTCTGATT TAAAGTTTCTGGATTGTCTTTGCTATTGGTCAAGAGCCAGCT
GGA GATGTTTCTGATT TAAAGTTTCTGGATTGTCTTTGCTATTGGTCAAGAGCCAGCT

TR      790     800     810     820     830     840
ATTHIREDB ACCAAGTTTTTGGATGGTGGTGTGAGTTAGATTGGATGGTTATGTTGTCAAGAGCCT
ACCAAGTTTTTGGATGGTGGTGTGAGTTAGATTGGATGGTTATGTTGTCAAGAGCCT

TR      850     860     870     880     890     900
ATTHIREDB GGTACTACACAGACTAGCGTCCCGGAGTTTTCGCTGCGGGTGATGTTCAAGGATAAGAAAG
GGTACTACACAGACTAGCGTCCCGGAGTTTTCGCTGCGGGTGATGTTCAAGGATAAGAAAG

TR      910     920     930     940     950     960
ATTHIREDB TATAGGCAAGCCATCACTGCTGCAGGAAGTGGTGCATGGCAGCTTTGGATGCAAGAGCAT
TATAGGCAAGCCATCACTGCTGCAGGAAGTGGTGCATGGCAGCTTTGGATGCAAGAGCAT

TR      970     980     990     1000    1010    1020
ATTHIREDB TACTTACAAAGAGATTGGATCTCAGCAAGGTAAGAGTGATTGA
TACTTACAAAGAGATTGGATCTCAGCAAGGTAAGAGTGATTGA

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1	ATG	AAT	GGT	CTC	GAA	ACT	CAC	AAC	ACA	AGG	CTC	TGT	ATC	GTA	GGA	AGT	GGC	CCA	GCG	GCA	60
1	M	N	G	L	E	T	H	N	T	R	L	C	I	V	G	S	G	P	A	A	20
61	CAC	ACG	GCG	GCG	ATT	TAC	GCA	GCT	AGG	GCT	GAA	CTT	AAA	CCT	CTT	CTC	TTC	GAA	GGA	TGG	120
21	H	T	A	A	I	Y	A	A	R	A	E	L	K	P	L	L	F	E	G	W	40
121	ATG	GCT	AAC	GAC	ATC	GCT	CCC	GGT	GGT	CAA	CTA	ACA	ACC	ACC	ACC	GAC	GTC	GAG	AAT	TTC	180
41	M	A	N	D	I	A	P	G	G	Q	L	T	T	T	T	D	V	E	N	F	60
181	CCC	GGA	TTT	CCA	GAA	GGT	ATT	CTC	GGA	GTA	GAG	CTC	ACT	GAC	AAA	TTC	CGT	AAA	CAA	TCG	240
61	P	G	F	P	E	G	I	L	G	V	E	L	T	D	K	F	R	K	Q	S	80
241	GAG	CGA	TTC	GGT	ACT	ACG	ATA	TTT	ACA	GAG	ACG	GTG	ACG	AAA	GTC	GAT	TTC	TCT	TCG	AAA	300
81	E	R	F	G	T	T	I	F	T	E	T	V	T	K	V	D	F	S	S	K	100
301	CCG	TTT	AAG	CTA	TTC	ACA	GAT	TCA	AAA	GCC	ATT	CTC	GCT	GAC	GCT	GTG	ATT	CTC	GCT	ACT	360
101	P	F	K	L	F	T	D	S	K	A	I	L	A	D	A	V	I	L	A	T	120
361	GGA	GCT	GTG	GCT	AAG	CGG	CTT	AGC	TTC	GTT	GGA	TCT	GGT	GAA	GGT	TCT	GGA	GGT	TTC	TGG	420
121	G	A	V	A	K	R	L	S	F	V	G	S	G	E	G	S	G	G	F	W	140
421	AAC	CGT	GGA	ATC	TCC	GCT	TGT	GCT	GTT	TGC	GAC	GGA	GCT	GCT	CCG	ATA	TTC	CGT	AAC	AAA	480
141	N	R	G	I	S	A	C	A	V	C	D	G	A	A	P	I	F	R	N	K	160
481	CCT	CTT	GCG	GTG	ATC	GGT	GGA	GGC	GAT	TCA	GCA	ATG	GAA	GAA	GCA	AAC	TTT	CTT	ACA	AAA	540
161	P	L	A	V	I	G	G	G	D	S	A	M	E	E	A	N	F	L	T	K	180
541	TAT	GGA	TCT	AAA	GTG	TAT	ATA	ATC	CAT	AGG	AGA	GAT	GCT	TTT	AGA	GCG	TCT	AAG	ATT	ATG	600
181	Y	G	S	K	V	Y	I	I	H	R	R	D	A	F	R	A	S	K	I	M	200
601	CAG	CAG	CGA	GCT	TTG	TCT	AAT	CCT	AAG	ATT	GAT	GTG	ATT	TGG	AAC	TCG	TCT	GTT	GTG	GAA	660
201	Q	Q	R	A	L	S	N	P	K	I	D	V	I	W	N	S	S	V	V	E	220
661	GCT	TAT	GGA	GAT	GGA	GAA	AGA	GAT	GTG	CTT	GGA	GGA	TTG	AAA	GTG	AAG	AAT	GTG	GTT	ACC	720
221	A	Y	G	D	G	E	R	D	V	L	G	G	L	K	V	K	N	V	V	T	240
721	GGA	GAT	GTT	TCT	GAT	TTA	AAA	GTT	TCT	GGA	TTG	TTC	TTT	GCT	ATT	GGT	CAT	GAG	CCA	GCT	780
241	G	D	V	S	D	L	K	V	S	G	L	F	F	A	I	G	H	E	P	A	260
781	ACC	AAG	TTT	TTG	GAT	GGT	GGT	GTT	GAG	TTA	GAT	TCG	GAT	GGT	TAT	GTT	GTC	ACG	AAG	CCT	840
261	T	K	F	L	D	G	G	V	E	L	D	S	D	G	Y	V	V	T	K	P	280
841	GGT	ACT	ACA	CAG	ACT	AGC	GTT	CCC	GGA	GTT	TTC	GCT	GCG	GGT	GAT	GTT	CAG	GAT	AAG	AAG	900
281	G	T	T	Q	T	S	V	P	G	V	F	A	A	G	D	V	Q	D	K	K	300
901	TAT	AGG	CAA	GCC	ATC	ACT	GCT	GCA	GGA	ACT	GGG	TGC	ATG	GCA	GCT	TT					

FIGURE 5

ClustalW Formatted Alignments

Translation of ATTHIREDB
Translation of TR

10 20 30 40 50 60
MNGLETHNTKLCIVGSGPAAHTAAIYAARAELEKPLELPEGWMAANDIAFGGQLNQPP-R-RENF
MNGLETHNTKLCIVGSGPAAHTAAIYAARAELEKPLELPEGWMAANDIAFGGQLNTTTDVENF

70 80 90 100 110 120
PGFPEGILGVELTDKFRKQSERFGTTTFTETVTKVDFSSKPPKLEFDSKAILADAVILA
PGFPEGILGVELTDKFRKQSERFGTTTFTETVTKVDFSSKPPKLEFDSKAILADAVILA

130 140 150 160 170 180
SAYAKWLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANPLTK
SAYAKWLSFVGSGEVSGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANPLTK

190 200 210 220 230 240
YGSKVYIIDRRDAFRASKIMQQRALS NPKIDVIWNSSVVEAYGDGERDVLGGGLKVKNVVT
YGSKVYIIDRRDAFRASKIMQQRALS NPKIDVIWNSSVVEAYGDGERDVLGGGLKVKNVVT

250 260 270 280 290 300
GUVS D L K V S G L F F A I G H E P A T K F L D G G V E L D S D G Y V V K P G L Q I S V P G V F A A G D V Q D K K
GUVS D L K V S G L F F A I G H E P A T K F L D G G V E L D S D G Y V V K P G L Q I S V P G V F A A G D V Q D K K

310 320 330 340 350 360
YRQA I T A A G T G C M A A L D A E H Y L Q E I G S Q Q G K S D
YRQA I T A A G T G C M A A L D A E H Y L Q E I G S Q Q G K S D

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FIGURE 6

PstI

1 ctgcaggaattcattgtactccagtatcattatagtgaaagtttggctctctcgcgggtgggtttttacctctattta 80

81 aaggggttttccacctaaaaattctgggtatcattctcactttacttggtactttaatttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataa 320

321 tgattttattcttattcttcttcatataaatgtttaatatatacaataataaacaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaataatttttcaaccacgtaaactctcataataataagttgtttcaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttatacaatgaaaatttcaccaaacaatcatttgggtattttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatgtgacactacggaagtaactgaagatctgcttttacatgagagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaatattacttttttaattttaagtttaattgttggaatttgtgactattgatttattattctactat 880

881 gtttaaatgtttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttacctaaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgcttttaccttttcttgggtatgtaagtcggaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttgggtcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttctactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactactactataata 1520

1521 ccccaacccaactcatattcaatactacttact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

00007000 00000000

FIGURE 6 (CONT'D)

1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG 1827
 72 S V A S D W A I Q A M P T F M F L K E G 91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA 1887
 92 K I L D K V V G A K K D E L Q S T I A K 111

HindIII

1888 CAC TTG GCT TAA gcttaataagtatgaactaaaatgcatgtaggtgaagagctcatggagagcatggaatattgt 1963
 112 H L A * 115

1964 atccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaggatgttatgatatattaa 2043

2044 cactctatctatgcaccttattgttctatgataaatttctcttattattataaatcatctgaatcgtgacggcttatgg 2123

2124 aatgcttcaaatagtacaaaaaacaatgtgtactataagactttctaaacaattctaaactttagcattgtgaacgagaca 2203

2204 taagtgttaagaagacataacaattataatggaagaagtttgtctcatttatataattatataactaccacttatgtatt 2283

2284 atattaggtgttaaggagacataacaattataaagagagaagtttgtatccatttatataattatataactaccatttat 2363

2364 atattatacttatccacttatttaagtctttataagggttgatccatgatatttctaataatttttagttgatatgtatat 2443

2444 gaaagggactattttgaactctcttactctgtataaagggttgatcatccttaaagtgggtctatttaattttattgtctt 2523

2524 cttacagataaaaaaaaaaattatgagttgggttgataaaatattgaaggattttaaataataataaataataaataacat 2603

2604 ataatatatgtatataaaatttattataatataacatttatctataaaaaagtaaattattgtcataaatctatacaatcgt 2683

2684 ttagccttgctggacgactctcaattatttaaacgagagtaaacaatatttgactttttgggtattttaacaaattattatt 2763

2764 taacactatatgaaattttttttttttatcggaaggaaataaaattaaattaggagggacaatgggtgtgtcccaatcct 2843

2844 tataacaaccaacttccacaggaaggtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggttgctc 2923

2924 ttgtttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatgggttgaccgtgtgcttag 3003

3004 cttcttttatttttattttttttatcagcaaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatac 3083

3084 aaaacccccaaaaacaagtttccttagcacccctaccaactaaggtagc 3129

KpnI

00007000:070501

FIGURE 7

PstI

1 ctgcaggaattcattgtactccagtatcattatagtgaaagttttggctctctcgccgggtggtttttacctctattta 80

81 aaggggttttccacctaaaaattctgggtatcattctcactttacttggtactttaatttctcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttggttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggtagaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaataaaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaaatataatttatcaaatatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacaccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaacaacatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaataactcaatattacttctaaaaaattaa 800

801 ttagatataaataaaatattacttttttaattttaagtttaattgttgaaattgtgactattgatttattattctactat 880

881 gtttaaatgttttatagatagtttaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgcttttaccttttcttgggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtgggtcttttggttcattgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaaagcaacacgtgcttaacatgcactttaaatgggtcaccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttcgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaataatcactcacttctttcatcatccatccatccagagtactactactactactataata 1520

1521 ccccaaccaactcatattcaataactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT 1587

1 M A D T A R G T H H D 11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC 1647

12 I I G R D Q Y P M M G R D R D Q Y Q M S 31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA 1707

32 G R G S D Y S K S R Q I A K A A T A V T 51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG 1767

52 A G G S L L V L S S L T L V G T V I A L 71

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[illegible]

1768	ACT	GTT	GCA	ACA	CCT	CTG	CTC	GTT	ATC	TTC	AGC	CCA	ATC	CTT	GTC	CCG	GCT	CTC	ATC	ACA	1827
72	T	V	A	T	P	L	L	V	I	F	S	P	I	L	V	P	A	L	I	T	91
1828	GTT	GCA	CTC	CTC	ATC	ACC	GGT	TTT	CTT	TCC	TCT	GGA	GGG	TTT	GGC	ATT	GCC	GCT	ATA	ACC	1887
92	V	A	L	L	I	T	G	F	L	S	S	G	G	F	G	I	A	A	I	T	111
1888	GTT	TTC	TCT	TGG	ATT	TAC	AA	<i>gtaagcacacat</i>												1960	
112	V	F	S	W	I	Y	K													118	
1961	<i>tgtgttgagccagtagcctttggatcaat</i>																				2040
2041	<i>catttgggttaactaaatacgaat</i>																				2120
2121	<i>ggatgataccctattgattgtgaatag</i>																				2184
119	G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG																				130
	Y A T G E H P Q G S D K																				
2185	TTG	GAC	AGT	GCA	AGG	ATG	AAG	TTG	GGA	AGC	AAA	GCT	CAG	GAT	CTG	AAA	GAC	AGA	GCT	CAG	2244
131	L	D	S	A	R	M	K	L	G	S	K	A	Q	D	L	K	D	R	A	Q	150
2245	TAC	TAC	GGA	CAG	CAA	CAT	ACT	GGT	GGG	GAA	CAT	GAC	CGT	GAC	CGT	ACT	CGT	GGT	GGC	CAG	2304
151	Y	Y	G	Q	Q	H	T	G	G	E	H	D	R	D	R	T	R	G	G	Q	170
	NcoI																				
2305	CAC	ACT	ACC	ATG	GCT	TCG	GAA	GAA	GGA	CAA	GTG	ATC	GCC	TGC	CAC	ACC	GTT	GAG	ACA	TGG	2364
171	H	T	T	M	A	S	E	E	G	Q	V	I	A	C	H	T	V	E	T	W	190
2365	AAC	GAG	CAG	CTT	CAG	AAG	GCT	AAT	GAA	TCC	AAA	ACT	CTT	GTG	GTG	GTT	GAT	TTC	ACG	GCT	2424
191	N	E	Q	L	Q	K	A	N	E	S	K	T	L	V	V	V	D	F	T	A	210
2425	TCT	TGG	TGT	GGA	CCA	TGT	CGT	TTC	ATC	GCT	CCA	TTC	TTT	GCT	GAT	TTG	GCT	AAG	AAA	CTT	2484
211	S	W	C	G	P	C	R	F	I	A	P	F	F	A	D	L	A	K	K	L	230
2485	CCT	AAC	GTG	CTT	TTC	CTC	AAG	GTT	GAT	ACT	GAT	GAA	TTG	AAG	TCG	GTG	GCA	AGT	GAT	TGG	2544
231	P	N	V	L	F	L	K	V	D	T	D	E	L	K	S	V	A	S	D	W	250
2545	GCG	ATA	CAG	GCG	ATG	CCA	ACC	TTC	ATG	TTT	TTG	AAG	GAA	GGG	AAG	ATT	TTG	GAC	AAA	GTT	2604
251	A	I	Q	A	M	P	T	F	M	F	L	K	E	G	K	I	L	D	K	V	270
2605	GTT	GGA	GCC	AAG	AAA	GAT	GAG	CTT	CAG	TCT	ACC	ATT	GCC	AAA	CAC	TTG	GCT	<i>TAA gcttaata</i>		2666	
271	V	G	A	K	K	D	E	L	Q	S	T	I	A	K	H	L	A	*		288	
2667	<i>agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataata</i>																				2746
2747	<i>actgagctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgt</i>																				2826
2827	<i>tctatgataaaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca</i>																				2906
2907	<i>aatgtgtactataagacttttctaacaattctaacttttagcattgtgaacgagacataagtgttaagaagacataacaat</i>																				2986
2987	<i>tataatggaagaagtttgtctccatttatattatatattaccacattatgtattatatattaggatgttaaggagacata</i>																				3066

[illegible]

KpnI

FIGURE 8

PstI

1 ctgcaggaatttcattgtactcccagtatcattatagtgaaggttttggtctctcgcgggtgggtttttacctctattta 80

81 aaggggttttccacctaataattctggtatcattctcactttacttgttactttaatttctcataatcttttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataataaacaattctttaccttaagaaggatttcccat 400

401 tttatatatttaaaaatatatttatcaaatatttttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacaccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataaataaataattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgcttttaccttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcaactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaataatcactcacttcttctcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC 1587

1 M A S E E G Q V I A C 11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG 1647

12 H T V E T W N E Q L Q K A N E S K T L V 31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT 1707

32 V V D F T A S W C G P C R F I A P F F A 51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG 1767

52 D L A K K L P N V L F L K V D T D E L K 71

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FIGURE 8 (CONT'D)

1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG 1827
72 S V A S D W A I Q A M P T F M F L K E G 91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA 1887
92 K I L D K V V G A K K D E L Q S T I A K 111

1888 CAC TTG GCT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG 1947
112 H L A M A D T A R G T H H D I I G R D Q 131

1948 TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC 2007
132 Y P M M G R D R D Q Y Q M S G R G S D Y 151

2008 TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT 2067
152 S K S R Q I A K A A T A V T A G G S L L 171

2068 GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG 2127
172 V L S S L T L V G T V I A L T V A T P L 191

2128 CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC 2187
192 L V I F S P I L V P A L I T V A L L I T 211

2188 GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC 2247
212 G F L S S G G F G I A A I T V F S W I Y 231

2248 AA *gtaagcacacatttatcatcttacttcataatcttctgtgcaatatgtgcatgtgttgagccagtagctttggat* 2326
232 K 232

2327 *caatcttttttggtcgaataacaaatgtaacaataagaaattgcaaattctaggaacatttggttaactaaatacgaat* 2406

2407 *ttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggtatgatacctattgattgtgaa* 2486

2487 *tag* G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG 2544
233 Y A T G E H P Q G S D K L D S A R M 250

2545 AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT 2604
251 K L G S K A Q D L K D R A Q Y Y G Q Q H 270

HindIII

2605 ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gcttaata 2666
271 T G G E H D R D R T R G G Q H T T * 288

2667 *agtatgaactaaaatgcatgtagggtgaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataata* 2746

2747 *actgagctccatctcacttcttcttatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgt* 2826

2827 *tctatgataaaatttctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca* 2906

2907 *aatgtgtactataagacttttctaacaatttctaacttttagcattgtgaacgagacataagtgttaagaagacataacaat* 2986

2987 *tataatggaagaagttgtctccatttatattatattatattaccacttatgtattatattaggatgttaaggagacata* 3066

[illegible]

KonI

FIGURE 9

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggttttttacctctattta 80

81 aaggggttttccacctaaaaattctgggtatcattctcactttacttgttactttaatttttcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggtagaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatataaaacaaattctttaccttaagaaggatttcccat 400

401 tttatatattttaaaaatatatttatcaaataatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacaccagtgacacaaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttatacaatgaaaatttcaccaaacaatcatttgggtattttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaaattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaagttagtagagtgttagagtgttaccctaaccataaac 960

961 tataagattttatgggtggactaattttcatatatttcttattgctttttaccttttcttggtatgtaagtcgcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttgggtcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttctactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaataactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587

1 M N G L E T H N T R L 11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647

12 C I V G S G P A A H T A A I Y A A R A E 31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707

32 L K P L L F E G W M A N D I A P G G Q L 51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767

52 T T T T D V E N F P G F P E G I L G V E 71

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FIGURE 9 (CONT'D)

1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG 1827
72 L T D K F R K Q S E R F G T T I F T E T 91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT 1887
92 V T K V D F S S K P F K L F T D S K A I 111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA 1947
112 L A D A V I L A T G A V A K R L S F V G 131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC 2007
132 S G E G S G G F W N R G I S A C A V C D 151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA 2067
152 G A A P I F R N K P L A V I G G G D S A 171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA 2127
172 M E E A N F L T K Y G S K V Y I I H R R 191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT 2187
192 D A F R A S K I M Q Q R A L S N P K I D 211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA 2247
212 V I W N S S V V E A Y G D G E R D V L G 231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG 2307
232 G L K V K N V V T G D V S D L K V S G L 251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT 2367
252 F F A I G H E P A T K F L D G G V E L D 271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC 2427
272 S D G Y V V T K P G T T Q T S V P G V F 291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG 2487
292 A A G D V Q D K K Y R Q A I T A A G T G 311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG 2547
312 C M A A L D A E H Y L Q E I G S Q Q G K 331

2548 AGT GAT TGA agctttaataagtatgaactaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatc 2624
332 S D * HindIII 334

2625 cgaccatgtaacagtataataaactgagctccatctcacttcttctatgaataaacaaggatgttatgatatattaacac 2704

2705 tctatctatgcaccttattgttctatgataaaatctcttattattataaatcatctgaatcgtgacggccttatggaat 2784

2785 gcttcaaatagtacaaaaacaaatgtgtactataagacttttctaacaattctaaacttttagcattgtgaacgagacataa 2864

2865 gtgttaagaagacataacaattataatggaagaagtttgtctccatttatattatattatattaccacttatgtattata 2944

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FIGURE 9 (CONT'D)

2945 ttaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatattatataactacccatttatata 3024
3025 ttatacttatccacttatttaagtgtctttataaggtttgatccatgatatttctaatttttagttgatatgtatatgaa 3104
3105 aggggtactatttgaactctcttactctgtataaagggttgatcatccttaaagtgggtctatttaattttattgcttctt 3184
3185 acagataaaaaaaaaattatgagttgggttgataaaatattgaaggatttaaaataataataaataaataaataacatata 3264
3265 atatatgtatataaaatttattataatataaacatttatctataaaaaagtaaatttgtcataaatctatacaatcgttta 3344
3345 gccttgctggacgactctcaattatttaaacgagagtaaacatatttgactttttggttatttaacaaattattatttaa 3424
3425 cactatatgaaattttttttttttatcggaaggaaataaaattaaattaggagggacaatgggtgtgtccaatccttat 3504
3505 acaaccaacttccacaggaagggtcaggtcggggacaacaaaaaacaggcaagggaattttttaatttgggtgtgtcttg 3584
3585 ttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatgggttgaccgtgtgcttagctt 3664
3665 cttttattttatttttttatcagcaaagaataaaataaaataaaatgagacacttcagggatgtttcaacccttatacaaa 3744
3745 accccaaaaacaagtttcctagcacccctaccaactaaggtacc 3787

KpnI

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FIGURE 10

PstI

1	ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggttttttacctctattta	80
81	aaggggtttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat	160
161	tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc	240
241	ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcggttgtagaaagcataa	320
321	tgatttattcttattcttcttcatataaatgtttaatatacaatatataacaaattctttaccttaagaaggatttcccat	400
401	tttatattttaaaaatatatttatcaaataatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa	480
481	aatttaactccataattttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat	560
561	aaaaaaatccaattatcattgtattttttttatacaatgaaaatttcaccaaacaatcatttgtgggtatttctgaagcaa	640
641	gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat	720
721	cttctaaagtaattttaataatagttactatatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa	800
801	ttagatataattaaaaattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat	880
881	gtttaaatgtttttatagatagtttaaagtaaatataagtaatgtagtagagtgtagagtgttaccctaaaccataaac	960
961	tataagatttatggtggactaattttcatatatttcttattgctttttaccttttcttgggtatgtaagtcgtaactggaa	1040
1041	ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaaag	1120
1121	aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc	1200
1201	catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaaccacacaca	1280
1281	aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttctactt	1360
1361	caacacacgtcaacctgcataatgcgtgtcatcccatgccccaaatctccatgcatttccaaccaccttctctcttatata	1440
1441	atacctataaatacctctataatcactcacttctttcatcatccatccatccagagtactactactctactactataata	1520
1521	ccccaaaccaactcatattcaatactactctact	1587
1	ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT	11
	M A D T A R G T H H D	
1588	ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC	1647
12	I I G R D Q Y P M M G R D R D Q Y Q M S	31
1648	GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA	1707
32	G R G S D Y S K S R Q I A K A A T A V T	51
1708	GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG	1767

FIGURE 10 (CONT'D)

52 A G G S L L V L S S L T L V G T V I A L 71

1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
72 T V A T P L L V I F S P I L V P A L I T 91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
92 V A L L I T G F L S S G G F G I A A I T 111

1888 GTT TTC TCT TGG ATT TAC AA *gtaagcacacatttatcatcttacttcataat* *tttgtgcaatatgtgcatgca* 1960
112 V F S W I Y K 118

1961 *tgtgttgagccagtagcctttggatcaat* *tttttttggtcgaataacaaatgtaacaataagaaattgcaaattc* *tagggaa* 2040

2041 *catttgggttaactaaatacgaat* *tttgacctagctagccttgaatgtgtctgtgtatatcatctatataggt* *aaaaatgctt* 2120

2121 *ggatgatacctattgattgtgaatag* G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG 2184
119 Y A T G E H P Q G S D K 130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
131 L D S A R M K L G S K A Q D L K D R A Q 150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
151 Y Y G Q Q H T G G E H D R D R T R G G Q 170

2305 CAC ACT ACC ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC TGT ATC GTA GGA AGT GGC 2364
171 H T T M N G L E T H N T R L C I V G S G 190

2365 CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA CTT AAA CCT CTT CTC TTC 2424
191 P A A H T A A I Y A A R A E L K P L L F 210

2425 GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA ACA ACC ACC ACC GAC GTC 2484
211 E G W M A N D I A P G G Q L T T T T D V 230

2485 GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG CTC ACT GAC AAA TTC CGT 2544
231 E N F P G F P E G I L G V E L T D K F R 250

2545 AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG GTG ACG AAA GTC GAT TTC 2604
251 K Q S E R F G T T I F T E T V T K V D F 270

2605 TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT CTC GCT GAC GCT GTG ATT 2664
271 S S K P F K L F T D S K A I L A D A V I 290

2665 CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA TCT GGT GAA GGT TCT GGA 2724
291 L A T G A V A K R L S F V G S G E G S G 310

2725 GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC GGA GCT GCT CCG ATA TTC 2784
311 G F W N R G I S A C A V C D G A A P I F 330

2785 CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA ATG GAA GAA GCA AAC TTT 2844
331 R N K P L A V I G G G D S A M E E A N F 350

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FIGURE 10 (CONT'D)

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2845 CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA GAT GCT TTT AGA GCG TCT 2904
351 L T K Y G S K V Y I I H R R D A F R A S 370

2905 AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT GTG ATT TGG AAC TCG TCT 2964
371 K I M Q Q R A L S N P K I D V I W N S S 390

2965 GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA GGA TTG AAA GTG AAG AAT 3024
391 V V E A Y G D G E R D V L G G L K V K N 410

3025 GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG TTC TTT GCT ATT GGT CAT 3084
411 V V T G D V S D L K V S G L F F A I G H 430

3085 GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT TCG GAT GGT TAT GTT GTC 3144
431 E P A T K F L D G G V E L D S D G Y V V 450

3145 ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC GCT GCG GGT GAT GTT CAG 3204
451 T K P G T T Q T S V P G V F A A G D V Q 470

3205 GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG TGC ATG GCA GCT TTG GAT 3264
471 D K K Y R Q A I T A A G T G C M A A L D 490

3265 GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG AGT GAT TGA agcttaataagt 3327
491 A E H Y L Q E I G S Q Q G K S D * HindIII 507

3328 atgaactaaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataaact 3407

3408 gagctccatctcacttcttctatgaataaacaaggatgttatgatataataacactctatctatgcaccttattgttct 3487

3488 atgataaatttctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaacaat 3567

3568 gtgtactataagactttctaaacaattctaacttttagcattgtgaacgagacataagtgtaagaagacataacaattat 3647

3648 aatggaagaagtttgtctccatttatataattatataattaccactttatgtattatattaggatgttaaggagacataaca 3727

3728 attataaagagagaagtttgtatccatttatataattatataactaccatttatataattataacttatccacttatttaag 3807

3808 tctttataaggtttgatccatgatatttctaataatttttagttgatatgtatatgaaaggtactatttgaactctcttac 3887

3888 tctgtataaagggttgatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaaattatgagt 3967

3968 tggtttgataaaatattgaaggattttaaataataataaataataaataacatataatatatgtatataaattttattata 4047

4048 atataacattttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaatta 4127

4128 tttaaacgagagtaaacatatatttgactttttggttatttaacaaattattatttaaacactatatgaaattttttttttt 4207

4208 atcggcaaggaaataaaaattaaattaggagggacaatgggtgtgtcccaatccttatacaaccaacttccacaggaaggtc 4287

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T05040-030600

FIGURE 10 (CONT'D)

4288 aggtcggggacaacaaaaaacaggcaagggaaatTTTTTaatttgggttgctctgtttgctgcataatttatgcagtaa 4367
4368 aacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttctttatTTTtatTTTTtatcagc 4447
4448 aaagaataaataaaaaataaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagca 4527
4528 ccctaccaactaaggtagc 4546
KpnI

105040-86846860

FIGURE 11

PstI

1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtgggttttttacctctattta 80

81 aagggggttttccacctaaaaattctgggtatcattctcactttactttgttactttaatttttcataatctttgggtgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggttagaaagcataa 320

321 tgattttattcttattcttcttcatataaaagttaaataacaataaaacaaattctttaccttaagaaggatttcccat 400

401 ttttatattttaaaaatatatttatcaaataattttcaaccacgtaaattctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccattttttctttgaat 560

561 aaaaaaatccaattatcattgtattttttttataacaatgaaaatttcaccaacaacatcatttgggtatttctgaagcaa 640

641 gtcattgttatgcaaaattctataattcccatgtgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaataactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttacctaaccataaac 960

961 tataagatttatgggtggactaattttcatatatttcttattgttttaccttttcttggtatgtaagtcgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttgggttcacatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatgggtcacccatctcaaccacacaca 1280

1281 aacacattgcctttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcggtgtcatcccatgccc aaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaaatacctctaataatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaaccaactcatattcaataactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC 1587

1 M N G L E T H N T R L 11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA 1647

12 C I V G S G P A A H T A A I Y A A R A E 31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA 1707

32 L K P L L F E G W M A N D I A P G G Q L 51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG 1767

52 T T T T D V E N F P G F P E G I L G V E 71

095289-0704

Figure 1. The 12 test patterns used in the experiment. The patterns are arranged in a 3x4 grid. Each pattern consists of a set of horizontal bars of varying lengths and positions, creating a unique visual stimulus for each of the 12 conditions.

Figure 1. The 12 test patterns used in the experiment. The patterns are arranged in a 3x4 grid. Each pattern consists of a set of horizontal bars of varying lengths and positions, creating a unique visual stimulus for each of the 12 conditions.

2728	CTC	TCC	AGC	CTT	ACC	CTT	GTT	GGA	ACT	GTC	ATA	GCT	TTG	ACT	GTT	GCA	ACA	CCT	CTG	CTC	2787	
392	L	S	S	L	T	L	V	G	T	V	I	A	L	T	V	A	T	P	L	L	411	
2788	GTT	ATC	TTC	AGC	CCA	ATC	CTT	GTC	CCG	GCT	CTC	ATC	ACA	GTT	GCA	CTC	CTC	ATC	ACC	GGT	2847	
412	V	I	F	S	P	I	L	V	P	A	L	I	T	V	A	L	L	I	T	G	431	
2848	TTT	CTT	TCC	TCT	GGA	GGG	TTT	GGC	ATT	GCC	GCT	ATA	ACC	GTT	TTC	TCT	TGG	ATT	TAC	AA	g	2907
432	F	L	S	S	G	G	F	G	I	A	A	I	T	V	F	S	W	I	Y	K	451	
2908	<i>taagcacacattttatcatcttacttcataatttttgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaat</i>																				2987	
2988	<i>ttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaaacattttggttaactaaatacgaaatttga</i>																				3067	
3068	<i>cctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaaatgcttggatatgatacctatttgattgtgaatag</i>																				3146	
3147	G	TAC	GCA	ACG	GGA	GAG	CAC	CCA	CAG	GGA	TCA	GAC	AAG	TTG	GAC	AGT	GCA	AGG	ATG	AAG	3204	
452	Y	A	T	G	E	H	P	Q	G	S	D	K	L	D	S	A	R	M	K		470	
3205	TTG	GGA	AGC	AAA	GCT	CAG	GAT	CTG	AAA	GAC	AGA	GCT	CAG	TAC	TAC	GGA	CAG	CAA	CAT	ACT	3264	
471	L	G	S	K	A	Q	D	L	K	D	R	A	Q	Y	Y	G	Q	Q	H	T	490	
3265	GGT	GGG	GAA	CAT	GAC	CGT	GAC	CGT	ACT	CGT	GGT	GGC	CAG	CAC	ACT	ACT	<u>TAA</u>	<u>gctt</u>	aataagta	3327		
491	G	G	E	H	D	R	D	R	T	R	G	G	Q	H	T	T	*	HindIII		507		
3328	<i>tgaactaaaaatgcatgtaggtgtaagagctcatggagagcatggaatatgttatccgaccatgtaacagtataataaactg</i>																				3407	
3408	<i>agctccatctcacttcttctatgaataaacaaggatgttatgatataattaacactctatctatgcaccttattgttcta</i>																				3487	
3488	<i>tgataaatttcctcttattattataaatcatctgaatcgtgacggccttatggaatgcttcaaatagtacaaaaacaaatg</i>																				3567	
3568	<i>tgtactataagacttttctaacaatttctaacttttagcattgtgaacgagacataaagtgttaagaagacataacaattata</i>																				3647	
3648	<i>atggaagaagtttgtctccatttatatattatatattaccacattatgtattatattaggatgttaaggagacataacaa</i>																				3727	
3728	<i>ttataaagagagaagtttgtatccatttatatattatataactaccacatttatatattatacttatccacttatttaatgt</i>																				3807	
3808	<i>ctttataagggttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctcttact</i>																				3887	
3888	<i>ctgtataaagggttgatcatccttaaagtggtctattttaattttattgcttcttacagataaaaaaaaaaattatgagtt</i>																				3967	
3968	<i>ggtttgataaaatattgaaggattttaaataataataaataaataaataacatataatatatgtatataaattttattataa</i>																				4047	
4048	<i>tataacatttatctataaaaaagtaaataattgtcataaaatctatacaatcgtttagccttgctggacgactctcaattat</i>																				4127	
4128	<i>ttaaacgagagtaaacatatttgacttttttggttatttaacaaattattatttaacactatatgaaatttttttttttta</i>																				4207	
4208	<i>tcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaagggtca</i>																				4287	

FIGURE 11 (CONT'D)

4288 ggtcggggacaacaaaaaacaggcaagggaaattttttaatttgggttgcttcttgctgcataatttatgcagtaaa 4367

4368 aactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttctttatttttttttatcagca 4447

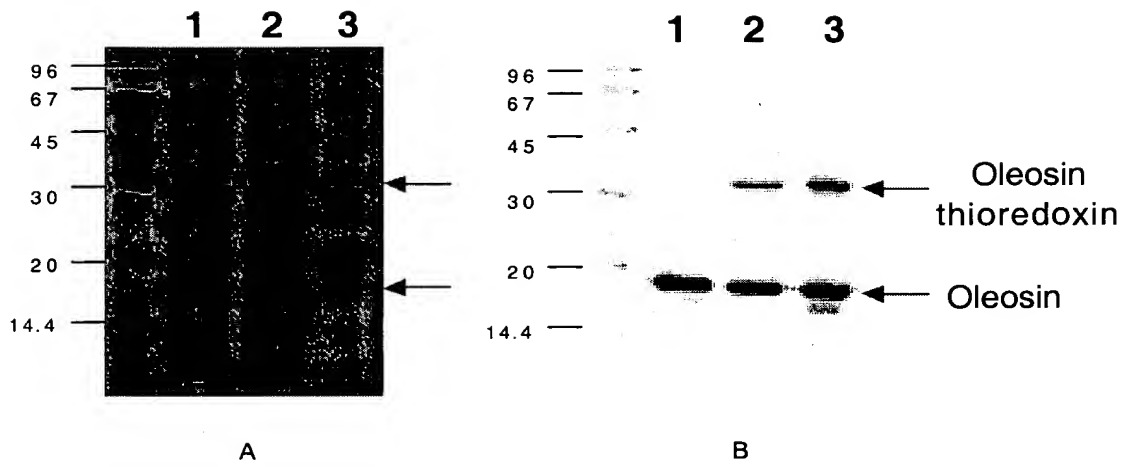
4448 aagaataaataaaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagcac 4527

4528 cctaccaactaaggtacc 4545

KpnI

0987898-070501
TDS020-86826860

FIGURE 12



09897898-070501

FIGURE 13

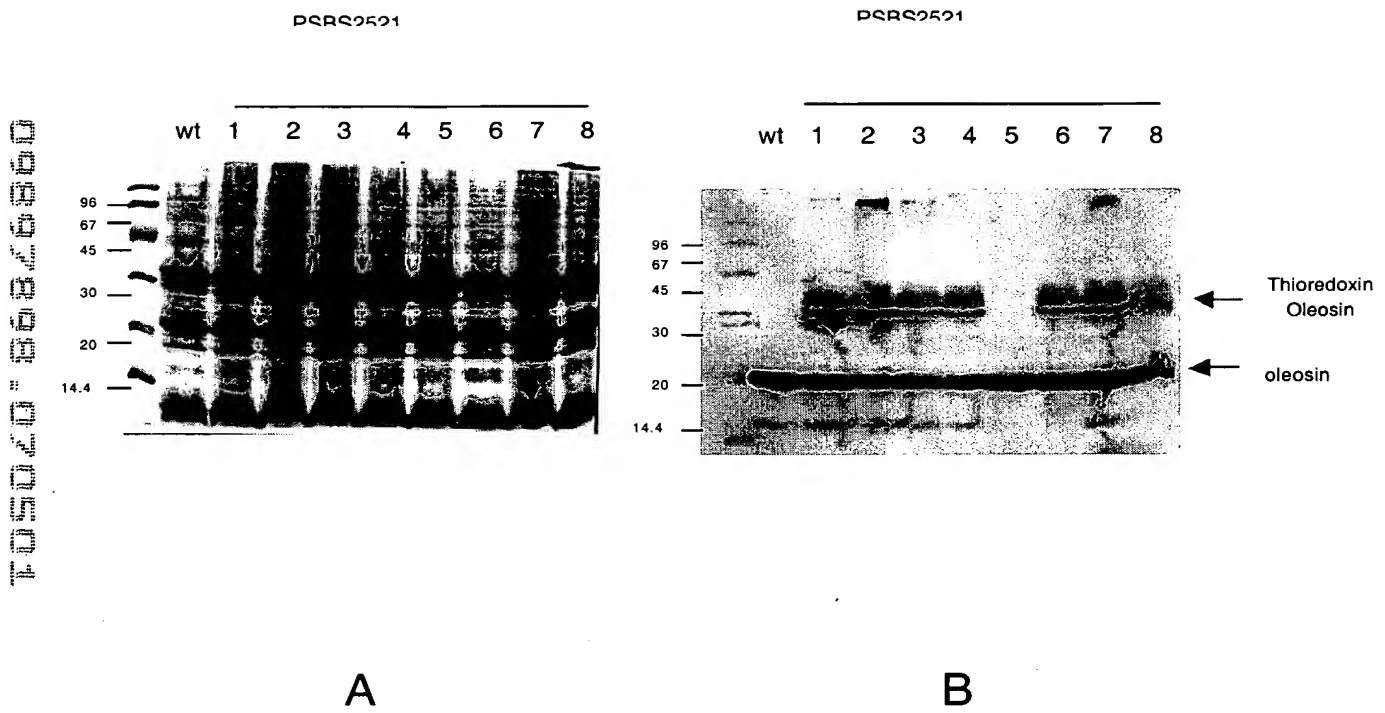


FIGURE 14

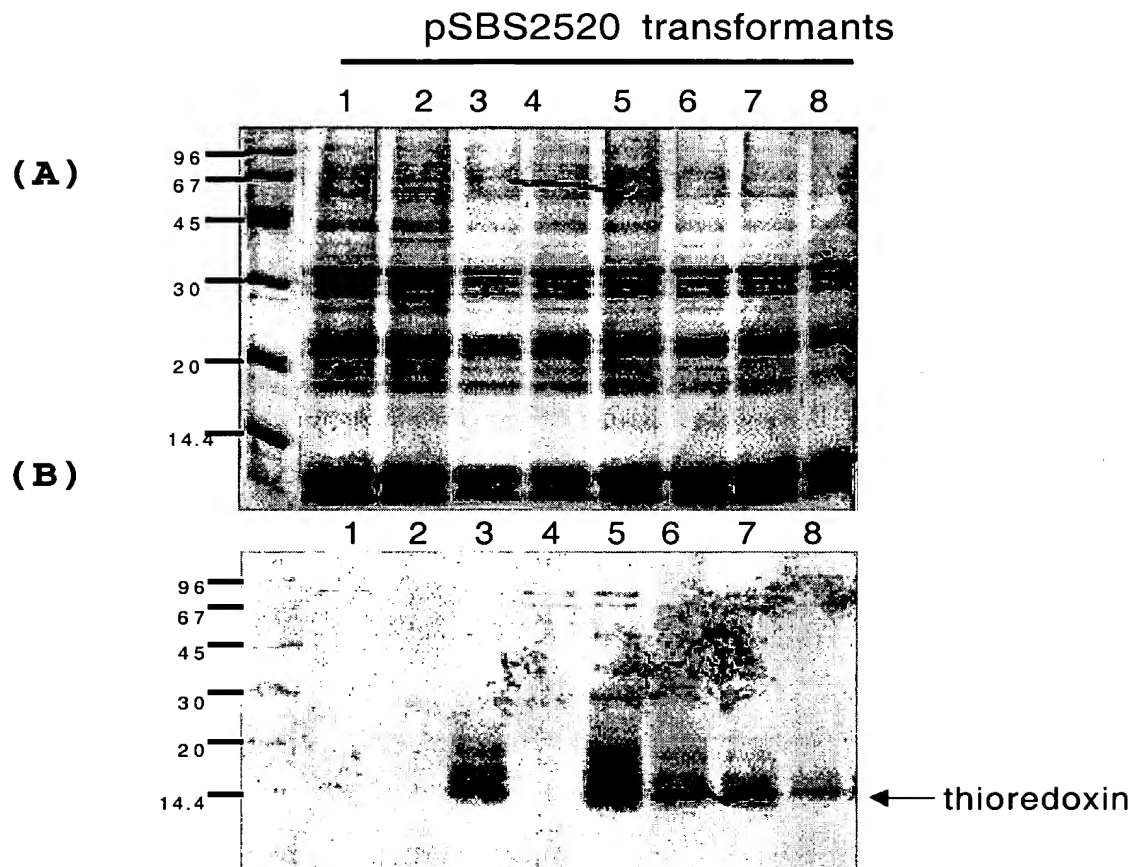
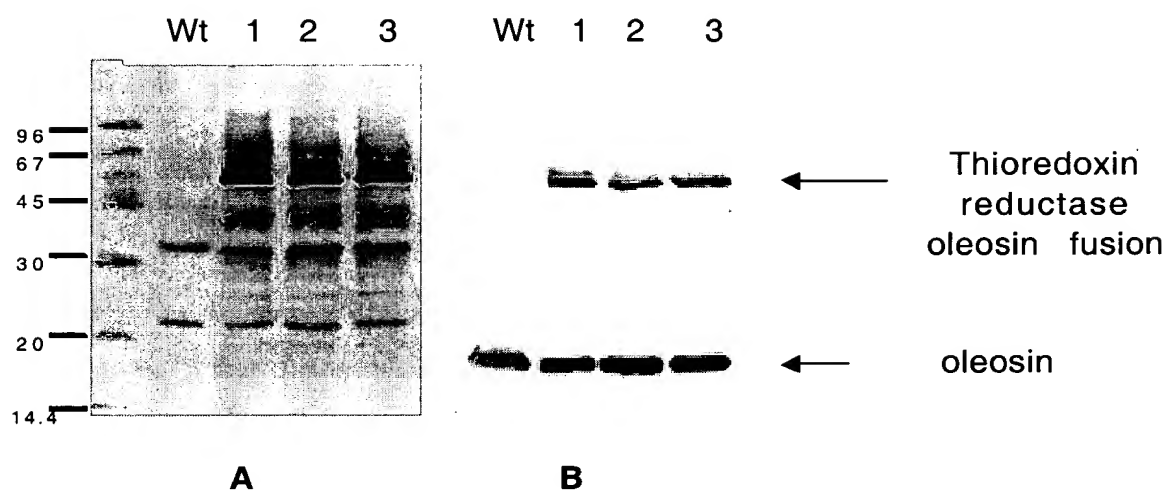
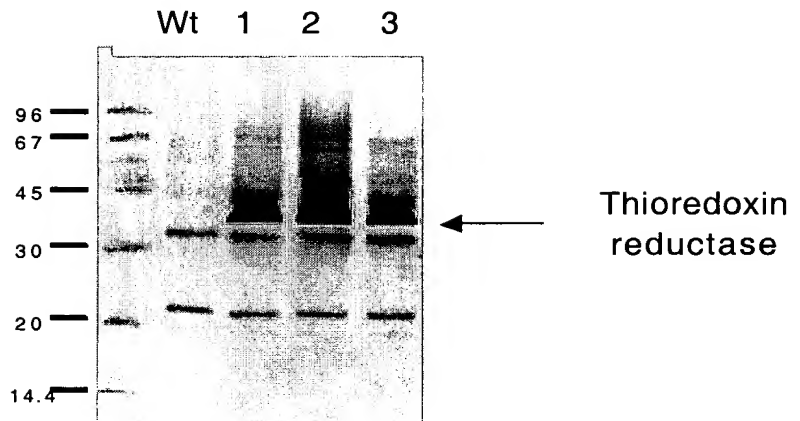


FIGURE 15



0807888:070501
T05020:86826860

FIGURE 16



105020 86826860

FIGURE 17

